



110	115	120	
tct cca gag acc atc gag gcc ctg cg a a g c c g a c c t t g a c g t c t g g Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	125	130	135
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag c a c a t g t a c c a c Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	140	145	150
gac ctc ggg ctg gtc agg gac ttc a g c a t c a a c c c t g t c a c c t c a g g Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	155	160	165
agg tgg ctg ttc tgc gtc c a c g a c a a c t a c a g a a a c c c c t t c c a c Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	170	175	180
a a c t t c c g g c a c t g c t t c g t g g c c a g a t g a t g t a c a g c a t g t c Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	190	195	200
tgg ctc tgc a g t c t c c a g a a g t t c t c a a a c g a t a t c c t g a t c Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile	205	210	215
c t a a t g a c a g c g a t c t g c c a c g a t c t g g a c c a t c c c g g c t a c a a c Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn	220	225	230
a a c a c g t a c c a g a a t g c c c g c a c a g a g c t g g c g g c t g c t a c a a t Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn	235	240	245
g a c a t c t c a c c g c t g g a a c c a c c a c t g c g c t t c c a g a t c Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile	250	255	260
c t c g c c g a g c c t g a a c a t c t t c a a c a t c c c a c t g a t g g g g Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly	270	275	280
t t c a a g c a g a t c c g a c a g g a t g a t c a c a t t a a t c t t g g c a c t g a c Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp	285	290	295
a t g g c a a g a c a t g c a g a a t t a t g g a t t c t t c a a a g a a a a t g g a g Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu	300	305	310
a a t t t g a c t a c a g c a a c g a g g a c a c a t g a c c c t g c t g a a g a t g a t t Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile	315	320	325
t t g a t a a a t g c t g t g a t a t c t c t a a c g a g g t c c g t c c a a t g g a a g t c Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val	330	335	340
			1060
			345

gca gag cct tgg gtg gac tgg tta tta gag gaa tat ttt atg cag agc Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser 350 355 360	1108
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg 365 370 375	1156
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val 380 385 390	1204
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu 395 400 405	1252
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu 410 415 420 425	1300
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp 430 435 440	1348
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp 445 450 455	1396
gtg aaa aac agt gaa gga gac tgg gcc tgaggaaagc gggggggcgtg Val Lys Asn Ser Glu Gly Asp Cys Ala 460 465	1443
gctgcagttc tggacgggct ggccgagctg cgcggatcc ttgtgcaggg aagagctgcc 1503	
ctggcacct ggcaccacaa gaccatgttt tctaagaacc atttt	1548
<210> 2	
<211> 466	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Asp Ala Phe Arg Ser Thr Pro Tyr Lys Val Arg Pro Val Ala Ile 1 5 10 15	
Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln 20 25 30	
Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala 35 40 45	
Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu 50 55 60	
Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys 65 70 75 80	

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys  
                   85                         90                         95  
  
 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp  
                   100                     105                         110  
  
 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala  
                   115                     120                         125  
  
 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met  
                   130                     135                         140  
  
 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp  
                   145                     150                         160  
  
 Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His  
                   165                     170                         175  
  
 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys  
                   180                     185                         190  
  
 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu  
                   195                     200                         205  
  
 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys  
                   210                     215                         220  
  
 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala  
                   225                     230                         240  
  
 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn  
                   245                     250                         255  
  
 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn  
                   260                     265                         270  
  
 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly  
                   275                     280                         285  
  
 Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile  
                   290                     295                         300  
  
 Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu  
                   305                     310                         320  
  
 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile  
                   325                     330                         335  
  
 Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys  
                   340                     345                         350  
  
 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly  
                   355                     360                         365  
  
 Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr  
                   370                     375                         380  
  
 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr

385 390 395 400  
Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu  
405 410 415  
Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala  
420 425 430  
Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr  
435 440 445  
Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp  
450 455 460  
Cys Ala  
465

<210> 3  
<211> 225  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<223> Nucleotides at positions 130, 186, and 205 are  
either A, T, G, or C.  
  
<400> 3  
agcgaccgtg agaagtccaga aggccttcct gtggAACCGT tcatggaccg agacaaagtg 60  
accaaggcca cagcccagat tgggttcatc aagtttgcgg tgatcccaat gtttgaaca 120  
gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180  
gatcgntacg aggagctgaa gcggntagat gacgcccata aagag 225  
  
<210> 4  
<211> 158  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<223> Nucleotides at positions 12, 36, 61, and 109 are  
either A, T, G, or C.  
  
<400> 4  
gtaccagatc antgccccca cagagctggc ggtccgntac aatgacatct caccgttgaa 60  
gnaaccacca ctgcgcgtg gccttcaga tcctcgccga gcctgagtg aacatcttct 120  
ccaacatccc acctgatggg ttcaaggaga tccgacag 158  
  
<210> 5  
<211> 98  
<212> DNA  
<213> Homo sapiens

1000 900 800 700 600 500 400 300 200 100

<220>  
<223> Nucleotides at positions 14, 22, and 50 are either  
A, T, C, or G.

<400> 5  
gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60  
ccaacatccc acctgatggg ttcaaggcaga tccgacag 98

<210> 6  
<211> 418  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Nucleotides at positions 1, 267, 352, 400, and 411  
are either A, T, G, or C.

<400> 6  
nggttaactg gcgcacatcttg tctttctctg agaacagcga tctggttatg gggcatttct 60  
gtctctaattg tcactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120  
ttcccggtgc cccgttcatg gaccgagaca aagtgaccaa gcccacagcc caggattggg 180  
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtg accaagctct tccccatggg 240  
ttgagggaga ttcatgctgg cagccantt gggaaatccc gaggattcgc tacgagggag 300  
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360  
acagtttga agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga 418

<210> 7  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,  
and 396 are either A, T, G, or C.

<400> 7  
nagaaaaaaag tgaacaaaaat ggttcttaga aaacatggc ttgtggtgcc aggtgcccag 60  
ggagactttc cctgcacaaag gntcccgccg antcggccag cccgtccaga actgcagcca 120  
cgccccccgn tttcctcagg cacagtctcc ttcactgttt ttacacatctc tgcttctctc 180  
tctggacttc tcggtgccccc cagacgtcaa gctgtcagtc ttcttctgtt actctttcat 240  
ggcggtcatc tatccgcttc agctcctcgt aggcgatctc gggattccc aaagtggct 300  
gcagcatgat cttcctcaac catggggggg aggagcttg ggcactngtt ttcaaaaatt 360  
gggggatcag gggacaaact ttgattggan cccatnttgg ggctttggg cctttgggc 420

aatttttg

428

<210> 8  
<211> 438  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Nucleotides at positions 63, 98, 107, 188, 203,  
206, 238, 252, 297, 370, 389, and 427 are either  
A, T, G, or C.

<400> 8  
ttttttttt tttttttgt atcagtgaac aaaatggttc ttagaaaaca tggctttgtg 60  
gtncagggtg cccagggagc tcttccctgc acaagganc cgcgcantcg gccagccgt 120  
ccagaactgc agccacgccc cccgtttcc tcagggcacag tctccttcac tgttttcac 180  
atctctgntt ctctctctgg gantntcgg tgggccccag aacgtcaagc tgtcagtnntt 240  
cttctgttaac ntnttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300  
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360  
gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaacccaatt 420  
tgggggntgt gggccttg 438

<210> 9  
<211> 262  
<212> DNA  
<213> Mus musculus

<400> 9  
gagaatttt actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaaa 60  
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120  
ttactggaag aatattttat gcagagtgc acgtgagaagt ccgaagcctt cctgtggccc 180  
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagttt 240  
tcctgatccc aatgtttgaa ac 262

<210> 10  
<211> 250  
<212> DNA  
<213> Mus musculus

<400> 10  
gagaatttt actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaaa 60  
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120

ttactggaaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180  
attcatggac cgagacaaag tgacccaaagc aacagccaaa ttgggttcat caagttgtc 240  
tgtccaaatgt 250

```
<210> 11
<211> 459
<212> DNA
<213> Homo sapiens
```

<220>  
<223> Nucleotides at positions 155, 393, and 442 are  
either A, T, G, or C.

```
<400> 11
attaatcttg gccactgaca tggcaagaca tgcagaaaatt atggattctt tcaaagagaa 60
aatggagaat ttgactaca gcaacggaga gcacatgacc ctggtgagtg gcttattctg 120
cctgggtggg cagccaggcg gttgggtgg cgaanagggtt catccatcca gctcacactg 180
gaagccaaga agctgaaaatt attagtcttc ttggaaacaag qtgtctataa atctggtttt 240
caagggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggtcctcct 300
tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360
aagtgggtg aaggccgtgc attctcgctc tgntttcca gagaattaaa accagtttc 420
ccttqaqqc acaqcccccaq cntqqcattt tqaaaqtg 459
```

<210> 12  
<211> 599  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (99) (443)

<400> 12  
tggccctcga ggccaagaat tcggcacgag tggttaactg gcgcacatcttg tctttctctg 60  
agaacacgca tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116  
Cys His Cys Leu Leu His  
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164  
 Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro  
 10 15 20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212  
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe  
25 30 35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc	260		
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe			
40	45	50	
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat	308		
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp			
55	60	65	70
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag	356		
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln			
75	80	85	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag	404		
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu			
90	95	100	
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc	453		
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala			
105	110	115	
ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg	513		
aagagctgcc ctggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca	573		
ctgataaaaa aaaaaaaaaa aaaaaaa	599		
<210> 13			
<211> 115			
<212> PRT			
<213> Homo sapiens			
<400> 13			
Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu			
1	5	10	15
Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala			
20	25	30	
Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu			
35	40	45	
Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro			
50	55	60	
Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp			
65	70	75	80
Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala			
85	90	95	
Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly			
100	105	110	
Asp Cys Ala			
115			

<210> 14  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 14  
agtcgaaattc accgtgagaa gtcagaag 28

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 15  
gtcaaagctt acatggtctt gtggtgcc 28

<210> 16  
<211> 1303  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (107)..(1066)

<400> 16  
agtgactcta ctttgtaaaa atgtgaaact tcgtgttaggt actcagtaaa tcagtaaatt 60  
cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115  
Ala Leu Glu  
1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163  
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro  
5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211  
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn  
20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259  
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met  
40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307  
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr  
55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355  
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His

70

75

80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg	85	90	95	403
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala				
gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg	100	105	110	451
Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val				
gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc	120	125	130	499
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile				
cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc	135	140	145	547
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile				
ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa	150	155	160	595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys				
gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg	165	170	175	643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu				
ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt	180	185	190	691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg				
cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat	200	205	210	739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr				
ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg	215	220	225	787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro				
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc	230	235	240	835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe				
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc	245	250	255	883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe				
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat	260	265	270	931
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp				
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag	280	285	290	979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln				
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag	295	300	305	1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu				

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc	1076										
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala											
310	315	320		ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg	1136	aagagctgcc ctgggcaccc ggcaccacaa gaccatgtt tctaagaacc attttggca	1196	ctgatacaaa aaaaaaaaaaag gaattcatga tgctgtacag aatttttattt taaaactgtc	1256	ttttaaataa tatattctta tacggaaaaa aaaaaaaaaaa aaaaaaaaaa	1303
320											
ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg	1136										
aagagctgcc ctgggcaccc ggcaccacaa gaccatgtt tctaagaacc attttggca	1196										
ctgatacaaa aaaaaaaaaaag gaattcatga tgctgtacag aatttttattt taaaactgtc	1256										
ttttaaataa tatattctta tacggaaaaa aaaaaaaaaaa aaaaaaaaaa	1303										

<210> 17  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 17																																																																											
Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser																																																																											
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10	15																																																																										
Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn																																																																											
20	25	30		Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala		35	40	45		Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe		50	55	60		Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp		65	70	75	80	Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr		85	90	95		Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His		100	105	110		Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe		115	120	125		Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile		130	135	140		Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp		145	150	155	160	Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His		165	170	175		Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn		180	185	190		Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu		195	200	205							
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Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe																																																																											
50	55	60		Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp		65	70	75	80	Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr		85	90	95		Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His		100	105	110		Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe		115	120	125		Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile		130	135	140		Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp		145	150	155	160	Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His		165	170	175		Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn		180	185	190		Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu		195	200	205																			
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Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp																																																																											
65	70	75	80	Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr		85	90	95		Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His		100	105	110		Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe		115	120	125		Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile		130	135	140		Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp		145	150	155	160	Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His		165	170	175		Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn		180	185	190		Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu		195	200	205																									
75	80																																																																										
Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr																																																																											
85	90	95		Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His		100	105	110		Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe		115	120	125		Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile		130	135	140		Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp		145	150	155	160	Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His		165	170	175		Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn		180	185	190		Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu		195	200	205																															
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Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His																																																																											
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Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe																																																																											
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Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile																																																																											
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Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp																																																																											
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Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn																																																																											
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Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro  
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 Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu  
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 Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys  
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 Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys  
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 ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg 253  
 Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met  
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 Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr  
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 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu  
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320

325

330

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Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp  
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Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu  
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1992-1993

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PDB ID: 1D2B

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Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn  
35 40 45  
Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp  
50 55 60  
Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro  
65 70 75 80  
Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val  
85 90 95  
Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu  
100 105 110  
Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val  
115 120 125  
Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp  
130 135 140  
Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn  
145 150 155 160  
Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro  
165 170 175  
Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr  
180 185 190  
Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro  
195 200 205  
Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu  
210 215 220  
Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe  
225 230 235 240  
Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His  
245 250 255  
Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser  
260 265 270  
Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

275

280

285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln  
290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro  
305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro  
325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile  
340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His  
355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr  
370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys  
385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp  
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Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg  
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